

EXHIBIT A



60240 SeqList 10.14.05.ST25
SEQUENCE LISTING

<110> The Trustees of Columbia University in the City of New York
Trakht, Ilya
Canfield, Robert
Kalantarov, Gary
Rudchenko, Sergei

<120> Novel Tumor-Associated Marker

<130> 0575/60240/JPW/AJM/AJD

<140> 09/664,958

<141> 2000-09-28

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<170> PatentIn version 3.3

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60240 SeqList 10.14.05.ST25

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<400> 8

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60240 SeqList 10.14.05.ST25

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Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu
35 40 45

Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Ser Asn Ser His Leu Arg
50 55 60

Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp Gly
65 70 75 80

Leu Lys Leu Met Leu Leu Leu Glu Phe Ile Ser Gly Glu Arg Leu Pro
85 90 95

Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val Asn
100 105 110

Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Ile Lys Leu Asp Phe His
115 120 125

Arg Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly Met
130 135 140

Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu
145 150 155 160

Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr
165 170 175

Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp Lys
180 185 190

Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu Leu
195 200 205

Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu Asn
210 215 220

Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu
225 230 235 240

Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala Ile
245 250 255

Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys
260 265 270

60240 SeqList 10.14.05.ST25

Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val
275 280 285

Asn Gln Glu Asn Cys Ser Thr Ser Met Glu Asp Tyr Glu Lys Leu Ala
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Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp
305 310 315 320

Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp
325 330 335

Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys
340 345 350

Cys Gln Leu Glu Ile Asn Phe Asn Ser Val Gln Thr Lys Leu Arg Leu
355 360 365

Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp
370 375 380

Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu
385 390 395 400

Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu
405 410 415

Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp
420 425 430

Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu
435 440 445

Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp
450 455 460

Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ser Ala Gln
465 470 475 480

Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg
485 490 495

Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His
500 505 510

Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile

Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro Ala Ala Pro Phe Asn
530 535 540

Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val
545 550 555 560

His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe
565 570 575

Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu His
580 585 590

Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser
595 600 605

Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys
610 615 620

Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu
625 630 635 640

Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu His Leu Arg Arg Gln
645 650 655

Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met
660 665 670

Glu Glu Ile Ala Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln
675 680 685

Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro
690 695 700

Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu
705 710 715 720

Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val
725 730 735

Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val
740 745 750

Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln
755 760 765

60240 SeqList 10.14.05.ST25

Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly
770 775 780

Gly Ala Leu Gly Arg Gly Val Gln Gly Leu Pro His Gln Pro Gly Leu
785 790 795 800

Arg Arg Gly Glu Arg Pro Ala Gly Glu Ala Glu Phe Asn Arg Ile Met
805 810 815

Ser Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe
820 825 830

Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln
835 840 845

Val Ile Thr Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr
850 855 860

Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys
865 870 875 880

Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Gly Val Arg Gly Ala
885 890 895

Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
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<213> Human

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60240 SeqList 10.14.05.ST25

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60240 SeqList 10.14.05.ST25

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<400> 10

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20 25 30

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Cys Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp
35 40 45

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Glu Asp Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile
50 55 60

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Ser Gly Glu Arg Leu Pro Lys Pro Glu Arg Gly Lys Met Arg Val His
65 70 75 80

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Lys Ile Asn Asn Val Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly
85 90 95

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Val Lys Leu Val Ser Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Ala
100 105 110

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Lys Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile
115 120 125

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Gln Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu
130 135 140

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Trp Cys Gln Arg Lys Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn
145 150 155 160

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Phe His Ile Ser Trp Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His
165 170 175

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60240 SeqList 10.14.05.ST25

Arg His Arg Pro Glu Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp
180 185 190

Pro Val Thr Asn Leu Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu
195 200 205

Asp Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg
210 215 220

Pro Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala
225 230 235 240

Phe Ser Gly Ala Gln Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys
245 250 255

Val Leu Ala Val Asn Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu
260 265 270

Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp
275 280 285

Leu Glu Asp Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys
290 295 300

Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val
305 310 315 320

Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys
325 330 335

Leu Arg Leu Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Asp Lys Met
340 345 350

Val Ser Asp Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys
355 360 365

Gly Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu
370 375 380

Asp His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Trp
385 390 395 400

Thr Asp Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala
405 410 415

Thr Leu Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu
420 425 430

60240 SeqList 10.14.05.ST25

Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile
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 Thr Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu
 465 470 475 480
 Thr His Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu
 485 490 495
 Ala Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe
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 515 520 525
 Val His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln
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 Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu
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 Ala Ile His Lys Glu Ala Gln Arg Ile Ala Glu Ser Asn His Ile Lys
 565 570 575
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 580 585 590
 Ser Lys Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala
 595 600 605
 Leu Leu Glu Glu Gln Ser Lys Gln Gln Ser Asn Glu His Leu Arg Arg
 610 615 620
 Gln Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys
 625 630 635 640
 Met Glu Glu Ile Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu Glu
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 Asp Gln Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr
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 Lys Pro Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu

Ala Leu Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile
690 695 700

Arg Val Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn
705 710 715 720

Glu Val Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln
725 730 735

Glu Gln Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp
740 745 750

His Gly Gly Ala Leu Gly Pro Glu Glu Phe Lys Ala Cys Leu Ile Ser
755 760 765

Leu Gly Tyr Asp Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe Asn
770 775 780

Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe
785 790 795 800

Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr
805 810 815

Ala Asp Gln Val Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys Asn
820 825 830

Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala
835 840 845

Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala Val
850 855 860

Pro Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu
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Ser Asp Leu

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<212> DNA
<213> Human

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60240 SeqList 10.14.05.ST25

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60240 SeqList 10.14.05.ST25

<212> PRT
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Arg Val Asn Val Ile His Ala Arg Gln Gln Val Arg Ser Pro Val Thr
      35      40      45

Asn Ile Ala Arg Thr Ser Phe Phe His Val Lys Arg Ser Asn Ile Trp
50      55      60

Leu Ala Ala Val Thr Lys Gln Asn Val Asn Ala Ala Met Val Phe Glu
65      70      75      80

Phe Leu Tyr Lys Met Cys Asp Val Met Ala Ala Tyr Phe Gly Lys Ile
      85      90      95

Ser Glu Glu Asn Ile Lys Asn Asn Phe Leu Leu Ile Tyr Glu Leu Leu
      100      105      110

Asp Glu Ile Leu Asp Phe Gly Tyr Pro Gln Asn Ser Glu Thr Gly Ala
      115      120      125

Leu Lys Thr Phe Ile Thr Gln Gln Gly Ile Lys Ser Gln His Gln Thr
      130      135      140

Lys Glu Glu Gln Ser Gln Ile Thr Ser Gln Val Thr Gly Gln Ile Gly
145      150      155      160

Trp Arg Arg Glu Gly Ile Lys Tyr Arg Arg Asn Glu Leu Phe Leu Asp
      165      170      175

Val Leu Glu Ser Val Asn Leu Leu Met Ser Pro Gln Gly Gln Val Leu
      180      185      190

Ser Ala His Val Ser Gly Arg Val Val Met Lys Ser Tyr Leu Ser Gly
      195      200      205

Met Pro Glu Cys Lys Phe Gly Met Asn Asp Lys Ile Val Ile Glu Lys
210      215      220

Gln Gly Lys Gly Thr Ala Asp Glu Thr Ser Lys Ser Gly Lys Gln Ser
225      230      235      240

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60240 SeqList 10.14.05.ST25

Ile Ala Ile Asp Asp Cys Thr Phe His Gln Cys Val Arg Leu Ser Lys
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 Glu Leu Met Arg Tyr Arg Thr Thr Lys Asp Ile Ile Leu Pro Phe Arg
 275 280 285
 Val Ile Pro Leu Val Arg Glu Val Gly Arg Thr Lys Leu Glu Val Lys
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 Val Val Ile Lys Ser Asn Phe Lys Pro Ser Leu Leu Ala Gln Lys Ile
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 Glu Val Arg Ile Pro Thr Pro Leu Asn Thr Ser Gly Val Gln Val Ile
 325 330 335
 Cys Met Lys Gly Lys Ala Lys Tyr Lys Ala Ser Glu Asn Ala Ile Val
 340 345 350
 Trp Lys Ile Lys Arg Met Ala Gly Met Lys Glu Ser Gln Ile Ser Ala
 355 360 365
 Glu Ile Glu Leu Leu Pro Thr Asn Asp Lys Lys Lys Trp Ala Arg Pro
 370 375 380
 Pro Ile Ser Met Asn Phe Glu Val Pro Phe Ala Pro Ser Gly Leu Lys
 385 390 395 400
 Val Arg Tyr Leu Lys Val Phe Glu Pro Lys Leu Asn Tyr Ser Asp His
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 Thr Arg Cys
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<212> PRT
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 Pro Pro Pro Pro Ala Leu Arg Pro Arg Leu Val Phe His Thr Gln Leu
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 Ala His Gly Ser Pro Thr Gly Arg Ile Glu Gly Phe Thr Asn Val Lys
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 Glu Leu Tyr Gly Lys Ile Ala Glu Ala Phe Arg Leu Pro Thr Ala Glu
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 Val Met Phe Cys Thr Leu Asn Thr His Lys Val Asp Met Asp Lys Leu
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 Leu Gly Gly Gln Ile Gly Leu Glu Asp Phe Ile Phe Ala His Val Lys
 115 120 125
 Gly Gln Arg Lys Glu Val Glu Val Phe Lys Ser Glu Asp Ala Leu Gly
 130 135 140
 Leu Thr Ile Thr Asp Asn Gly Ala Gly Tyr Ala Phe Ile Lys Arg Ile
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 Lys Glu Gly Ser Val Ile Asp His Ile His Leu Ile Ser Val Gly Asp
 165 170 175
 Met Ile Glu Ala Ile Asn Gly Gln Ser Leu Leu Gly Cys Arg His Tyr
 180 185 190
 Glu Val Ala Arg Leu Leu Lys Glu Leu Pro Arg Gly Arg Thr Phe Thr
 195 200 205
 Leu Lys Leu Thr Glu Pro Arg Lys Ala Phe Asp Met Ile Ser Gln Arg
 210 215 220
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245

250

255

Pro Ser Ala Phe Glu Glu Lys Ala Ile Glu Lys Val Asp Asp Leu Leu
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Glu Ser Tyr Met Gly Ile Arg Asp Thr Glu Leu Ala Ala Thr Met Val
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Glu Leu Gly Lys Asp Lys Arg Asn Pro Asp Glu Leu Ala Glu Ala Leu
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<400> 16

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 35 40 45

Leu Ala Ser Glu Lys Ser Glu Met Gln Arg His Tyr Val Met Tyr Tyr
 50 55 60

Glu Met Ser Tyr Gly Leu Asn Ile Glu Met His Lys Gln Ala Glu Ile
 65 70 75 80

Val Lys Arg Leu Asn Gly Ile Cys Ala Gln Val Leu Pro Tyr Leu Ser
 85 90 95

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Gln Glu His Gln Gln Gln Val Leu Gly Ala Ile Glu Arg Ala Lys Gln
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Val Thr Ala Pro Glu Leu Asn Ser Ile Ile Arg Gln Gln Leu Gln Ala
 115 120 125

His Gln Leu Ser Gln Leu Gln Ala Leu Ala Leu Pro Leu Thr Pro Leu
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Pro Val Gly Leu Gln Pro Pro Ser Leu Pro Ala Val Ser Ala Gly Thr
 145 150 155 160

Gly Leu Leu Ser Leu Ser Ala Leu Gly Ser Gln Ala His Leu Ser Lys
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Glu Lys Ser Asp
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60240 SeqList 10.14.05.ST25

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 <211> 197
 <212> PRT
 <213> Human

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Phe Gln Leu Leu Gln Ala Gln Tyr His Ser Leu Lys Leu Glu Cys Asp
 35 40 45

Lys Leu Ala Ser Glu Lys Ser Glu Met Gln Arg His Tyr Val Met Tyr
 50 55 60

Tyr Glu Met Ser Tyr Gly Leu Asn Ile Glu Met His Lys Gln Ala Glu
 65 70 75 80

Ile Val Lys Arg Leu Asn Gly Ile Cys Ala Gln Val Leu Pro Tyr Leu
 85 90 95

Ser Gln Glu His Gln Gln Gln Val Leu Gly Ala Ile Glu Arg Ala Lys
 100 105 110

60240 SeqList 10.14.05.ST25

Gln Val Thr Ala Pro Glu Leu Asn Ser Ile Ile Arg Gln Gln Leu Gln
 115 120 125

Ala His Gln Leu Ser Gln Leu Gln Ala Leu Ala Leu Pro Leu Thr Pro
 130 135 140

Leu Pro Val Gly Leu Gln Pro Pro Ser Leu Pro Ala Val Ser Ala Gly
 145 150 155 160

Thr Gly Leu Leu Ser Leu Ser Ala Leu Gly Ser Gln Ala His Leu Ser
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Lys Glu Asp Lys Asn Gly His Asp Gly Asp Thr His Gln Glu Asp Asp
 180 185 190

Gly Glu Lys Ser Asp
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<210> 19
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 <213> Human

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Gly Arg Gly Glu Val Ile Thr Thr Tyr Cys Pro Ala Asn Asn Glu Pro
35 40 45

Ile Ala Arg Val Arg Gln Ala Ser Val Ala Asp Tyr Glu Glu Thr Val
50 55 60

Lys Lys Ala Arg Glu Ala Trp Lys Ile Trp Ala Asp Ile Pro Ala Pro
65 70 75 80

Lys Arg Gly Glu Ile Val Arg Gln Ile Gly Asp Ala Leu Arg Glu Lys
85 90 95

Ile Gln Val Leu Gly Ser Leu Val Ser Leu Glu Met Gly Lys Ile Leu
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100

105

110

Val Glu Gly Val Gly Glu Val Gln Glu Tyr Val Asp Ile Cys Asp Tyr
 115 120 125
 Ala Val Gly Leu Ser Arg Met Ile Gly Gly Pro Ile Leu Pro Ser Glu
 130 135 140
 Arg Ser Gly His Ala Leu Ile Glu Gln Trp Asn Pro Val Gly Leu Val
 145 150 155 160
 Gly Ile Ile Thr Ala Phe Asn Phe Pro Val Ala Val Tyr Gly Trp Asn
 165 170 175
 Asn Ala Ile Ala Met Ile Cys Gly Asn Val Cys Leu Trp Lys Gly Ala
 180 185 190
 Pro Thr Thr Ser Leu Ile Ser Val Ala Val Thr Lys Ile Ile Ala Lys
 195 200 205
 Val Leu Glu Asp Asn Lys Leu Pro Gly Ala Ile Cys Ser Leu Thr Cys
 210 215 220
 Gly Gly Ala Asp Ile Gly Thr Ala Met Ala Lys Asp Glu Arg Val Asn
 225 230 235 240
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 245 250 255
 Met Val Gln Glu Arg Phe Gly Arg Ser Leu Leu Glu Leu Gly Gly Asn
 260 265 270
 Asn Ala Ile Ile Ala Phe Glu Asp Ala Asp Leu Ser Leu Val Val Pro
 275 280 285
 Ser Ala Leu Phe Ala Ala Val Gly Thr Ala Gly Gln Arg Cys Thr Thr
 290 295 300
 Ala Arg Arg Leu Phe Ile His Glu Ser Ile His Asp Glu Val Val Asn
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 Arg Leu Lys Lys Ala Tyr Ala Gln Ile Arg Val Gly Asn Pro Trp Asp
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 Pro Asn Val Leu Tyr Gly Pro Leu His Thr Lys Gln Ala Val Ser Met
 340 345 350

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Tyr Gly Gly Lys Val Met Asp Arg Pro Gly Asn Tyr Val Glu Pro Thr
 370 375 380

Ile Val Thr Gly Leu Gly His Asp Ala Ser Ile Ala His Thr Glu Thr
 385 390 395 400

Phe Ala Pro Ile Leu Tyr Val Phe Lys Phe Lys Asn Glu Glu Glu Val
 405 410 415

Phe Ala Trp Asn Asn Glu Val Lys Gln Gly Leu Ser Ser Ser Ile Phe
 420 425 430

Thr Lys Asp Leu Gly Arg Ile Phe Arg Trp Leu Gly Pro Lys Gly Ser
 435 440 445

Asp Cys Gly Ile Val Asn Val Asn Ile Pro Thr Ser Gly Ala Glu Ile
 450 455 460

Gly Gly Ala Phe Gly Gly Glu Lys His Thr Gly Gly Gly Arg Glu Ser
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 <212> PRT
 <213> Human

<400> 22

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			20					25					30		
His	Ile	Tyr	Glu	Lys	Ser	Gly	Ala	Lys	Trp	Thr	Lys	Val	His	Glu	Leu
		35					40					45			
Lys	Glu	His	Asn	Gly	Gln	Val	Thr	Gly	Ile	Asp	Trp	Ala	Pro	Glu	Ser
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 145 150 155 160
 Ser Cys Asp Phe Lys Cys Arg Ile Phe Ser Ala Tyr Ile Lys Glu Val
 165 170 175
 Glu Glu Arg Pro Ala Pro Thr Pro Trp Gly Ser Lys Met Pro Phe Gly
 180 185 190
 Glu Leu Met Phe Glu Ser Ser Ser Ser Cys Gly Trp Val His Gly Val
 195 200 205
 Cys Phe Ser Ala Ser Gly Ser Arg Val Ala Trp Val Ser His Asp Ser
 210 215 220
 Thr Val Cys Leu Ala Asp Ala Asp Lys Lys Met Ala Val Ala Thr Leu
 225 230 235 240
 Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu Thr Phe Ile Thr Asp Asn
 245 250 255
 Ser Leu Val Ala Ala Gly His Asp Cys Phe Pro Val Leu Phe Thr Tyr
 260 265 270
 Asp Ala Ala Ala Gly Met Leu Ser Phe Gly Gly Arg Leu Asp Val Pro
 275 280 285
 Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala Arg Glu Arg Phe Gln Asn
 290 295 300
 Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly Thr Ala Ala Gly Ala Gly
 305 310 315 320
 Leu Asp Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser
 325 330 335
 Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly
 340 345 350

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Gly Met Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp
 355 360 365

Leu Lys Ile Lys
 370

<210> 23
 <211> 1435
 <212> DNA
 <213> Human

<400> 23
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 caccacgttc accaagatct tcgtgggagg cctgccgtac cacactaccg acgcctcgct 120
 caggaagtac ttcgagggct tcggcgacat cgaggaggcc gtggtcatca ccgaccgcca 180
 gacgggcaag tcccgcggct acggcttcgt gaccatggcc gaccgggagg cagctgagag 240
 ggcttgcaaa gaccctaacc ccatcatcga cggccgcaag gccaacgtga acctggcata 300
 tctgggagcc aagccttggt gtctccagac gggctttgcc attggcgctg agcagctgca 360
 cccaccttg atccagcggg cttacgggct gaccccgac tacatctacc caccagccat 420
 cgtgcagcca agcgtggtga tcccagccgc ccctgtcccg tcgctgtcct cgccctacat 480
 tgagtacacg ccggccagcc cggctctacg ccagtacca ccggccacct atgaccagta 540
 cccatacgcc gcctcgctg ccacggctga cagcttcgtg ggctacagct accctgccgc 600
 cgtgcaccag gccctctcag ccgcagcacc cgcgggcacc actttcgtgc agtaccaggc 660
 gccgcagctg cagcctgaca ggatgcagtg agggggcgtt ctgccccgag gactgtggca 720
 ttgtcacctt cacagcagac agagctgcca ggccatgatg ggctggcgac agcccggctg 780
 agcttcagtg aggtgccacc agcaccctg cctccgaaga ccgctcgggc attccgcctg 840
 cgccctggga cagcggagag acggcttctc tttaatctag gtcccattgt gtcttgaggg 900
 aggactttta agaatgactg agaactatth aaagacgcaa tcccagggtc cttgcacacc 960
 atggcagcct ctccttgac cttctcctgc ctctccacac tccagggtcc ctcaggcttg 1020
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 tattgtaact tgatcctccc gagctgtgag cgcagtctga ggtctgagga cacggcctcc 1200
 tggtggagtc ccattttctc catcagggca cgtgggaggc ttcctcaagc ccggaggagc 1260
 tcccaggcgc acaggggagg ccggtaacag gggccgagg ccaaaggccc ctttccagtc 1320
 atagcactga agttgcaact tttttcttgt aattgttttg ctactaagat aatttcagaa 1380
 gttcagtcta ttttttcagc ggatactgcc gccaccaaga atccaaacct aggaa 1435

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<210> 24
 <211> 230
 <212> PRT
 <213> Human

<400> 24

Ser Ala Gly Phe Ser Arg Pro Leu Ala Ala Pro Gly Val Met Tyr Gly
 1 5 10 15

Ser Gln Lys Gly Thr Thr Phe Thr Lys Ile Phe Val Gly Gly Leu Pro
 20 25 30

Tyr His Thr Thr Asp Ala Ser Leu Arg Lys Tyr Phe Glu Gly Phe Gly
 35 40 45

Asp Ile Glu Glu Ala Val Val Ile Thr Asp Arg Gln Thr Gly Lys Ser
 50 55 60

Arg Gly Tyr Gly Phe Val Thr Met Ala Asp Arg Ala Ala Ala Glu Arg
 65 70 75 80

Ala Cys Lys Asp Pro Asn Pro Ile Ile Asp Gly Arg Lys Ala Asn Val
 85 90 95

Asn Leu Ala Tyr Leu Gly Ala Lys Pro Trp Cys Leu Gln Thr Gly Phe
 100 105 110

Ala Ile Gly Val Gln Gln Leu His Pro Thr Leu Ile Gln Arg Thr Tyr
 115 120 125

Gly Leu Thr Pro His Tyr Ile Tyr Pro Pro Ala Ile Val Gln Pro Ser
 130 135 140

Val Val Ile Pro Ala Ala Ala Pro Val Pro Ser Leu Ser Ser Pro Tyr
 145 150 155 160

Ile Glu Tyr Thr Pro Ala Ser Pro Val Tyr Ala Gln Tyr Pro Pro Ala
 165 170 175

Thr Tyr Asp Gln Tyr Pro Tyr Ala Ala Ser Pro Ala Thr Ala Asp Ser
 180 185 190

Phe Val Gly Tyr Ser Tyr Pro Ala Ala Val His Gln Ala Leu Ser Ala
 195 200 205

Ala Ala Pro Ala Gly Thr Thr Phe Val Gln Tyr Gln Ala Pro Gln Leu
 210 215 220

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Gln Pro Asp Arg Met Gln
225 230

<210> 25
<211> 1439
<212> DNA
<213> Human

<400> 25
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gctcaggaag tacttcgagg gcttcggcga catcgaggag gccgtggtca tcaccgaccg 180
ccagacgggc aagtcccgcg gctacggctt cgtgaccatg gccgaccggg cggcagctga 240
gagggccttg aaagaccctt aaccccatca tcgacggccg caaggccaac gtgaacctgg 300
catatctggg cgccaagcct tgggtgtctcc agacgggctt tgccattggc gtgcagcagc 360
tgcacccac cttgatccag cggacttacg ggctgacccc gcactacatc taccaccag 420
ccatcgtgca gcccagcgtg gtgatcccag ccgcccctgt cccgtcgtg tcctcgcctt 480
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agtaccata cgccgcctcg cctgccacgg ctgacagctt cgtgggctac agctaccctg 600
ccgccgtgca ccaggccctc tcagccgcag caccgcggg caccactttc gtgcagtacc 660
aggcgccgca gctgcagcct gacaggatgc agtgaggggc gttcctgccc cgaggactgt 720
ggcattgtca ccttcacagc agacagagct gccaggccat gatgggctgg cgacagcccg 780
gctgagcttc agtgagggtg caccagcacc cgtgcctccg aagaccgctc gggcattccg 840
cctgcgcctt gggacagcgg agagacggct tctctttaat ctaggtccca ttgtgtcttg 900
agggaggact tttaagaatg actgagaact atttggggac gcaatcccag gttccttgca 960
caccatggca gcctctcctt gcaccttctc ctgcctctcc aactccagg ttccctcagg 1020
cttgtgtccc cactgctgca tcgtggcggg gtgtcacaga ccctctgcag cccctggctg 1080
ccctggactg tgcagagatg cctgactcca gggaaacctg aaagcaagaa gttaatggac 1140
tgtttattgt aacttgatcc tcccagctg tgagcgcagt ctgaggctg aggacacggc 1200
ctcctgttgg agtcccattt tctccatcag ggcacgtggg cggcttcctc aagcccggag 1260
gagctcccag gcgcacaggg gccgccggtg acaggggccc ccggccaaag gcccctttcc 1320
agtcatagca ctgaagttgc aacttttttc ttgtaattgt tttgctacta agataatttc 1380
agaagttcag tctatTTTTT cagcggatac tgccgccacc aagaatccaa acctaggaa 1439

<210> 26
<211> 230
<212> PRT

<213> Human

<400> 26

Arg Arg Met Gln Tyr Asn Arg Arg Phe Val Asn Val Val Pro Thr Phe
 1 5 10 15

Gly Lys Lys Lys Gly Thr Thr Phe Thr Lys Ile Phe Val Gly Gly Leu
 20 25 30

Pro Tyr His Thr Thr Asp Ala Ser Leu Arg Lys Tyr Phe Glu Gly Phe
 35 40 45

Gly Asp Ile Glu Glu Ala Val Val Ile Thr Asp Arg Gln Thr Gly Lys
 50 55 60

Ser Arg Gly Tyr Gly Phe Val Thr Met Ala Asp Arg Ala Ala Ala Glu
 65 70 75 80

Arg Ala Cys Lys Asp Pro Asn Pro Ile Ile Asp Gly Arg Lys Ala Asn
 85 90 95

Val Asn Leu Ala Tyr Leu Gly Ala Lys Pro Trp Cys Leu Gln Thr Gly
 100 105 110

Phe Ala Ile Gly Val Gln Gln Leu His Pro Thr Leu Ile Gln Arg Thr
 115 120 125

Tyr Gly Leu Thr Pro His Tyr Ile Tyr Pro Pro Ala Ile Val Gln Pro
 130 135 140

Ser Val Val Ile Pro Ala Ala Pro Val Pro Ser Leu Ser Ser Pro Tyr
 145 150 155 160

Ile Glu Tyr Thr Pro Ala Ser Pro Val Tyr Ala Gln Tyr Pro Pro Ala
 165 170 175

Thr Tyr Asp Gln Tyr Pro Tyr Ala Ala Ser Pro Ala Thr Ala Asp Ser
 180 185 190

Phe Val Gly Tyr Ser Tyr Pro Ala Ala Val His Gln Ala Leu Ser Ala
 195 200 205

Ala Ala Pro Ala Gly Thr Thr Phe Val Gln Tyr Gln Ala Pro Gln Leu
 210 215 220

Gln Pro Asp Arg Met Gln
 225 230

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<210> 27
 <211> 2029
 <212> DNA
 <213> 27

<400> 27
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 ccgactccga gcagtctctg tccttcgacc cgagccccgc gccctttccg ggacccctgc 180
 cccgcgggca gcgctgccaa cctgccggcc atggagaccc cgtcccagcg gcgcgccacc 240
 cgcagcgggg cgaggccag ctccactccg ctgtcggcca cccgcatcac ccggctgcag 300
 gagaaggagg acctgcagga gctcaatgat cgcttggcgg tctacatcga ccgtgtgcgc 360
 tcgctggaaa cggagaacgc agggctgcgc cttcgcatca ccgagtctga agagggtgtc 420
 agccgcgagg tgtccggcat caaggccgcc tacgaggccg agctcgggga tgcccgaag 480
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 gaggagttta aggagctgaa agcgcgcaat accaagaagg aggggtgacct gatagctgct 600
 caggctcggc tgaaggacct ggaggctctg ctgaactcca aggaggccgc actgagcact 660
 gctctcagtg agaagcgcac gctggagggc gagctgcatg atctgcgggg ccagggtggc 720
 aagcttgagg cagccctagg tgaggccaag aagcaacttc aggatgagat gctgcggcgg 780
 gtggatgctg agaacaggct gcagaccatg aaggaggaac tggacttcca gaagaacatc 840
 tacagtgagg agctgcgtga gaccaagcgc cgtcatgaga cccgactggt ggagattgac 900
 aatgggaagc agcgtgagtt tgagagccgg ctggcggatg cgctgcagga actgcggggc 960
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 ctggacattg ccaggcagtc tgctgagagg aacagcaacc tgggtggggc tgcccacgag 1080
 gagctgcagc agtcgcgcat ccgcatcgac agcctctctg cccagctcag ccagctccag 1140
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 cgggacacca gccggcggct gctggcggaa aaggagcggg agatggccga gatgcgggca 1260
 aggatgcagc agcagctgga cgagtaccag gagcttcttg acatcaagct ggccctggac 1320
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 cccagcccta cctcgcagcg cagccgtggc cgtgcttcct ctactcatc ccagacacag 1440
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 tcacagcacg cacgcactag cgggcgcgtg gccgtggagg aggtggatga ggagggcaag 1560
 tttgtccggc tgcgcaacaa gtccaatgag gaccagtcca tgggcaattg gcagatcaag 1620
 cgccagaatg gagatgatcc cttgctgact taccggttcc caccaaagtt caccctgaag 1680

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gctgggcagg tggtgacgat ctgggctgca ggagctgggg ccaccacacag cccccctacc 1740
gacctggtgt ggaaggcaca gaacacctgg ggctgcggga acagcctgcg tacggctctc 1800
atcaactcca ctggggaaga agtggccatg cgcaagctgg tgcgctcagt gactgtgggtt 1860
gaggacgacg aggatgagga tggagatgac ctgctccatc accaccatgt gagtggtagc 1920
cgccgctgag gccgagcctg cactggggcc acccagccag gcctgggggc agcctctccc 1980
cagcctcccc gtgccaaaaa tcttttcatt aaagaatggtt tggaacttt 2029

<210> 28
<211> 572
<212> PRT
<213> Human

<400> 28

Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala
1 5 10 15

Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
20 25 30

Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
35 40 45

Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
50 55 60

Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
65 70 75 80

Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala
85 90 95

Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu
100 105 110

Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile
115 120 125

Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys
130 135 140

Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly
145 150 155 160

Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu
165 170 175

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Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp
 180 185 190
 Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys
 195 200 205
 Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr
 210 215 220
 Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg
 225 230 235 240
 Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val
 245 250 255
 Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp
 260 265 270
 Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala
 275 280 285
 His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala
 290 295 300
 Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu
 305 310 315 320
 Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg
 325 330 335
 Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met
 340 345 350
 Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala
 355 360 365
 Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu
 370 375 380
 Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly
 385 390 395 400
 Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr
 405 410 415
 Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln
 420 425 430

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His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu
435 440 445

Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met
450 455 460

Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr
465 470 475 480

Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr
485 490 495

Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu
500 505 510

Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr
515 520 525

Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val
530 535 540

Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp
545 550 555 560

Leu Leu His His His His Val Ser Gly Ser Arg Arg
565 570

<210> 29
<211> 10
<212> PRT
<213> Human

<400> 29

Asn Leu Leu Glu Lys Asp Tyr Phe Gly Leu
1 5 10

<210> 30
<211> 10
<212> PRT
<213> Human

<400> 30

Val Leu Phe Asp Leu Val Cys Glu His Leu
1 5 10

<210> 31
<211> 9
<212> PRT

<213> Human

<400> 31

Lys Leu Gln His Pro Asp Met Leu Val
 1 5

<210> 32

<211> 9

<212> PRT

<213> Human

<400> 32

Lys Met Leu Asp Ala Glu Asp Ile Val
 1 5

<210> 33

<211> 10

<212> PRT

<213> Human

<400> 33

Lys Met Thr Leu Gly Met Ile Trp Thr Ile
 1 5 10

<210> 34

<211> 9

<212> PRT

<213> Human

<400> 34

Phe Met Pro Ser Glu Gly Lys Met Val
 1 5

<210> 35

<211> 10

<212> PRT

<213> Human

<400> 35

Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile
 1 5 10

<210> 36

<211> 9

<212> PRT

<213> Human

<400> 36

Gly Leu Val Thr Phe Gln Ala Phe Ile
 1 5

<210> 37
 <211> 10
 <212> PRT
 <213> Human

<400> 37

Cys Gln Leu Glu Ile Asn Phe Asn Ser Val
 1 5 10

<210> 38
 <211> 10
 <212> PRT
 <213> Human

<400> 38

Trp Leu Ala Ala Val Thr Lys Gln Asn Val
 1 5 10

<210> 39
 <211> 10
 <212> PRT
 <213> Human

<400> 39

Ile Leu Pro Phe Arg Val Ile Pro Leu Val
 1 5 10

<210> 40
 <211> 9
 <212> PRT
 <213> Human

<400> 40

Ser Leu Leu Ala Gln Lys Ile Glu Val
 1 5

<210> 41
 <211> 9
 <212> PRT
 <213> Human

<400> 41

Lys Leu Asn Tyr Ser Asp His Asp Val
 1 5

<210> 42
 <211> 9
 <212> PRT
 <213> Human

<400> 42

Lys Leu Leu Gly Gly Gln Ile Gly Leu

1 5

<210> 43
 <211> 10
 <212> PRT
 <213> Human

<400> 43

Ser Leu Leu Gly Cys Arg His Tyr Glu Val
 1 5 10

<210> 44
 <211> 10
 <212> PRT
 <213> Human

<400> 44

Tyr Leu Ser Gln Glu His Gln Gln Gln Val
 1 5 10

<210> 45
 <211> 10
 <212> PRT
 <213> Human

<400> 45

Lys Val Met Asp Arg Pro Gly Asn Tyr Val
 1 5 10

<210> 46
 <211> 9
 <212> PRT
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<400> 46

Ala Leu Ile Glu Gln Trp Asn Pro Val
 1 5

<210> 47
 <211> 9
 <212> PRT
 <213> Human

<400> 47

Ile Ile Thr Ala Phe Asn Phe Pro Val
 1 5

<210> 48
 <211> 9
 <212> PRT
 <213> Human

<400> 48

Phe Glu Gln Glu Asn Asp Trp Trp Val
1 5

<210> 49

<211> 9

<212> PRT

<213> Human

<400> 49

Tyr Leu Gly Ala Lys Pro Trp Cys Leu
1 5

<210> 50

<211> 10

<212> PRT

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<400> 50

Cys Leu Gln Thr Gly Phe Ala Ile Gly Val
1 5 10

<210> 51

<211> 10

<212> PRT

<213> Human

<400> 51

Lys Leu Leu Glu Gly Glu Glu Glu Arg Leu
1 5 10

<210> 52

<211> 9

<212> PRT

<213> Human

<400> 52

Lys Leu Val Arg Ser Val Thr Val Val
1 5

<210> 53

<211> 9

<212> PRT

<213> Human

<400> 53

Arg Leu Ala Asp Ala Leu Gln Glu Leu
1 5